

RAW SEQUENCE LISTING

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Application Serial Number: 10/520,258A
Source: IFWO
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IFWO

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DATE: 04/03/2006

PATENT APPLICATION: US/10/520,258A

TIME: 15:13:12

Input Set : A:\20050-00003.ST25.txt

Output Set: N:\CRF4\04032006\J520258A.raw

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3 <110> APPLICANT: NEXGEN BIOTECHNOLOGIES, INC.
4     SHONG, Min-Ho
5     LEE, Sun
6     YOO, Jae-Geun
7     JIN, Seok-Min
9 <120> TITLE OF INVENTION: Production of Transformed Plants Expressing Thyroid
Stimulating
10     Hormone Receptor
12 <130> FILE REFERENCE: 20050-00003
14 <140> CURRENT APPLICATION NUMBER: US 10/520,258A
C--> 15 <141> CURRENT FILING DATE: 2005-01-03
17 <150> PRIOR APPLICATION NUMBER: KR 2002-38064
18 <151> PRIOR FILING DATE: 2002-07-02
20 <150> PRIOR APPLICATION NUMBER: PCT/KR2003/001308
21 <151> PRIOR FILING DATE: 2003-07-02
23 <160> NUMBER OF SEQ ID NOS: 5
25 <170> SOFTWARE: PatentIn version 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2292
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(2289)
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40 1          5          10          15
42 agg gac ctg ggc gga atg ggg tgt tcg tct cca ccc tgc gag tgc cat      96
43 Arg Asp Leu Gly Gly Met Gly Cys Ser Ser Pro Pro Cys Glu Cys His
44          20          25          30
46 cag gag gag gac ttc aga gtc acc tgc aag gat att caa cgc atc ccc      144
47 Gln Glu Glu Asp Phe Arg Val Thr Cys Lys Asp Ile Gln Arg Ile Pro
48          35          40          45
50 agc tta ccg ccc agt acg cag act ctg aag ctt att gag act cac ctg      192
51 Ser Leu Pro Pro Ser Thr Gln Thr Leu Lys Leu Ile Glu Thr His Leu
52          50          55          60
54 aga act att cca agt cat gca ttt tct aat ctg ccc aat att tcc aga      240
55 Arg Thr Ile Pro Ser His Ala Phe Ser Asn Leu Pro Asn Ile Ser Arg
56 65          70          75          80
58 atc tac gta tct ata gat gtg act ctg cag cag ctg gaa tca cac tcc      288
59 Ile Tyr Val Ser Ile Asp Val Thr Leu Gln Gln Leu Glu Ser His Ser
60          85          90          95
62 ttc tac aat ttg agt aaa gtg act cac ata gaa att cgg aat acc agg      336

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63	Phe	Tyr	Asn	Leu	Ser	Lys	Val	Thr	His	Ile	Glu	Ile	Arg	Asn	Thr	Arg	
64				100					105					110			
66	aac	tta	act	tac	ata	gac	cct	gat	gcc	ctc	aaa	gag	ctc	ccc	ctc	cta	384
67	Asn	Leu	Thr	Tyr	Ile	Asp	Pro	Asp	Ala	Leu	Lys	Glu	Leu	Pro	Leu	Leu	
68			115					120					125				
70	aag	tcc	ttg	gca	ttt	tca	aac	act	gga	ctt	aaa	atg	ttc	cct	gac	ctg	432
71	Lys	Ser	Leu	Ala	Phe	Ser	Asn	Thr	Gly	Leu	Lys	Met	Phe	Pro	Asp	Leu	
72		130					135				140						
74	acc	aaa	gtt	tat	tcc	act	gat	ata	ttc	ttt	ata	ctt	gaa	att	aca	gac	480
75	Thr	Lys	Val	Tyr	Ser	Thr	Asp	Ile	Phe	Phe	Ile	Leu	Glu	Ile	Thr	Asp	
76	145				150				155				160				
78	aac	cct	tac	atg	acg	tca	atc	cct	gtg	aat	gct	ttt	cag	gga	cta	tgc	528
79	Asn	Pro	Tyr	Met	Thr	Ser	Ile	Pro	Val	Asn	Ala	Phe	Gln	Gly	Leu	Cys	
80				165					170				175				
82	aat	gaa	acc	ttg	aca	ctg	aag	ctg	tac	aac	aat	ggc	ttt	act	tca	gtc	576
83	Asn	Glu	Thr	Leu	Thr	Leu	Lys	Leu	Tyr	Asn	Asn	Gly	Phe	Thr	Ser	Val	
84			180					185				190					
86	caa	gga	tat	gat	ttc	ttt	ggg	aca	aag	ctg	gat	gct	gtt	tac	cta	aac	624
87	Gln	Gly	Tyr	Asp	Phe	Phe	Gly	Thr	Lys	Leu	Asp	Ala	Val	Tyr	Leu	Asn	
88		195				200			205								
90	aag	aat	aaa	tac	ctg	aca	gtt	att	gac	aaa	gat	gca	ttt	gga	gga	gta	672
91	Lys	Asn	Lys	Tyr	Leu	Thr	Val	Ile	Asp	Lys	Asp	Ala	Phe	Gly	Gly	Val	
92		210				215			220								
94	tac	agt	gga	cca	agc	ttg	ctg	gac	gtg	tct	caa	acc	agt	gtc	act	gcc	720
95	Tyr	Ser	Gly	Pro	Ser	Leu	Leu	Asp	Val	Ser	Gln	Thr	Ser	Val	Thr	Ala	
96	225			230				235				240					
98	ctt	cca	tcc	aaa	ggc	ctg	gag	cac	ctg	aag	gaa	ctg	ata	gca	aga	aac	768
99	Leu	Pro	Ser	Lys	Gly	Leu	Glu	His	Leu	Lys	Glu	Leu	Ile	Ala	Arg	Asn	
100				245				250				255					
102	agc	tgg	act	ctt	aag	aaa	ctt	gca	ctt	tcc	ttg	agt	ttc	ctt	cac	ctc	816
103	Ser	Trp	Thr	Leu	Lys	Lys	Leu	Ala	Leu	Ser	Leu	Ser	Phe	Leu	His	Leu	
104			260					265				270					
106	aca	cgg	gct	gac	ctt	tct	tac	cca	agc	cac	tgc	tgt	gct	ttt	aag	aat	864
107	Thr	Arg	Ala	Asp	Leu	Ser	Tyr	Pro	Ser	His	Cys	Cys	Ala	Phe	Lys	Asn	
108		275				280			285								
110	cag	aag	aaa	atc	aga	gga	atc	ctt	gag	tcc	ttg	atg	tgt	aat	gag	agc	912
111	Gln	Lys	Lys	Ile	Arg	Gly	Ile	Leu	Glu	Ser	Leu	Met	Cys	Asn	Glu	Ser	
112		290				295			300								
114	agt	atc	gag	acg	ttg	cgc	cag	aga	aaa	tct	gtg	aat	gcc	ttg	aat	agc	960
115	Ser	Ile	Glu	Thr	Leu	Arg	Gln	Arg	Lys	Ser	Val	Asn	Ala	Leu	Asn	Ser	
116	305			310				315				320					
118	ccc	ctc	cac	cag	gaa	tat	gaa	gag	aat	ctg	ggt	gac	agc	att	gtt	ggg	1008
119	Pro	Leu	His	Gln	Glu	Tyr	Glu	Glu	Asn	Leu	Gly	Asp	Ser	Ile	Val	Gly	
120				325				330				335					
122	tac	aag	gaa	aag	tcc	aag	ttc	cag	gat	act	cat	aac	aac	gct	cat	tat	1056
123	Tyr	Lys	Glu	Lys	Ser	Lys	Phe	Gln	Asp	Thr	His	Asn	Asn	Ala	His	Tyr	
124		340						345				350					
126	tac	gtc	ttc	ttt	gaa	gaa	caa	gag	gat	gag	atc	att	ggt	ttt	ggc	cag	1104
127	Tyr	Val	Phe	Phe	Glu	Glu	Gln	Glu	Asp	Glu	Ile	Ile	Gly	Phe	Gly	Gln	

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131	Glu Leu Lys Asn Pro Gln Glu Glu Thr Leu Gln Ala Phe Asp Ser His			
132	370 375 380			
134	tat gac tac acc ata tgt ggg gac agt gaa gac atg gtg tgt acc ccc	1200		
135	Tyr Asp Tyr Thr Ile Cys Gly Asp Ser Glu Asp Met Val Cys Thr Pro			
136	385 390 395 400			
138	aag tcc gat gag ttc aac ccg tgt gaa gac ata atg ggc tac aag ttc	1248		
139	Lys Ser Asp Glu Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Lys Phe			
140	405 410 415			
142	ctg aga att gtg gtg tgg ttc gtt agt ctg ctg gct ctc ctg ggc aat	1296		
143	Leu Arg Ile Val Val Trp Phe Val Ser Leu Leu Ala Leu Gly Asn			
144	420 425 430			
146	gtc ttt gtc ctg ctt att ctc ctc acc agc cac tac aaa ctg aac gtc	1344		
147	Val Phe Val Leu Leu Ile Leu Leu Thr Ser His Tyr Lys Leu Asn Val			
148	435 440 445			
150	ccc cgc ttt ctc atg tgc aac ctg gcc ttt gcg gat ttc tgc atg ggg	1392		
151	Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp Phe Cys Met Gly			
152	450 455 460			
154	atg tac ctg ctc ctc atc gcc tct gta gac ctc tac act cac tct gag	1440		
155	Met Tyr Leu Leu Leu Ile Ala Ser Val Asp Leu Tyr Thr His Ser Glu			
156	465 470 475 480			
158	tac tac aac cat gcc atc gac tgg cag aca ggc cct ggg tgc aac acg	1488		
159	Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Pro Gly Cys Asn Thr			
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162	gct ggt ttc ttc act gtc ttt gca agc gag tta tcg gtg tat acg ctg	1536		
163	Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu			
164	500 505 510			
166	acg gtc atc acc ctg gag cgc tgg tat gcc atc acc ttc gcc atg gcc	1584		
167	Thr Val Ile Thr Leu Glu Arg Trp Tyr Ala Ile Thr Phe Ala Met Ala			
168	515 520 525			
170	ctg gac cgg aag atc cgc ctc agg cac gca tgt gcc atc atg gtt ggg	1632		
171	Leu Asp Arg Lys Ile Arg Leu Arg His Ala Cys Ala Ile Met Val Gly			
172	530 535 540			
174	ggc tgg gtt tgc tgc ttc ctt ctc gcc ctg ctt cct ttg gtg gga ata	1680		
175	Gly Trp Val Cys Cys Phe Leu Leu Ala Leu Leu Pro Leu Val Gly Ile			
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178	agt agc tat gcc aaa gtc agt atc tgc ctg ccc atg gac acc gag acc	1728		
179	Ser Ser Tyr Ala Lys Val Ser Ile Cys Leu Pro Met Asp Thr Glu Thr			
180	565 570 575			
182	cct ctt gct ctg gca tat att gtt ttt gtt ctg acg ctc aac ata gtt	1776		
183	Pro Leu Ala Leu Ala Tyr Ile Val Phe Val Leu Thr Leu Asn Ile Val			
184	580 585 590			
186	gcc ttc gtc atc gtc tgc tgc tgt tat gtg aag atc tac atc aca gtc	1824		
187	Ala Phe Val Ile Val Cys Cys Tyr Val Lys Ile Tyr Ile Thr Val			
188	595 600 605			
190	cga aat ccg cac aac cca ggg gac aaa gat acc aaa att gcc aag agg	1872		
191	Arg Asn Pro His Asn Pro Gly Asp Lys Asp Thr Lys Ile Ala Lys Arg			
192	610 615 620			

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196 625          630          635          640
198 ttc tat gct gtg tca gca att ctg aac aag cct ctc atc act gtt agc      1968
199 Phe Tyr Ala Val Ser Ala Ile Leu Asn Lys Pro Leu Ile Thr Val Ser
200          645          650          655
202 aac tcc aaa atc ttg ctg gta ctc ttc tat cca att aac tcc tgt gcc      2016
203 Asn Ser Lys Ile Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala
204          660          665          670
206 aat cca ttc ctc tat gct att ttc acc aag gcc ttc cag agg gat gtg      2064
207 Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Ala Phe Gln Arg Asp Val
208          675          680          685
210 ttc atc cta ctc agc aag ttt ggc atc tgt aaa cgc cag gct cag gca      2112
211 Phe Ile Leu Leu Ser Lys Phe Gly Ile Cys Lys Arg Gln Ala Gln Ala
212          690          695          700
214 tac cgg ggg cag agg gtt cct cca aag aac agc act gat att cag gtt      2160
215 Tyr Arg Gly Gln Arg Val Pro Pro Lys Asn Ser Thr Asp Ile Gln Val
216 705          710          715          720
218 caa aag gtt acc cac gac atg agg cag ggt ctc cac aac atg gaa gat      2208
219 Gln Lys Val Thr His Asp Met Arg Gln Gly Leu His Asn Met Glu Asp
220          725          730          735
222 gtc tat gaa ctg att gaa aac tcc cat cta acc cca aag aag caa ggc      2256
223 Val Tyr Glu Leu Ile Glu Asn Ser His Leu Thr Pro Lys Lys Gln Gly
224          740          745          750
226 caa atc tca gaa gag tat atg caa acg gtt ttg taa      2292
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233 <212> TYPE: PRT
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243          20          25          30
246 Gln Glu Glu Asp Phe Arg Val Thr Cys Lys Asp Ile Gln Arg Ile Pro
247          35          40          45
250 Ser Leu Pro Pro Ser Thr Gln Thr Leu Lys Leu Ile Glu Thr His Leu
251          50          55          60
254 Arg Thr Ile Pro Ser His Ala Phe Ser Asn Leu Pro Asn Ile Ser Arg
255 65          70          75          80
258 Ile Tyr Val Ser Ile Asp Val Thr Leu Gln Leu Glu Ser His Ser
259          85          90          95
262 Phe Tyr Asn Leu Ser Lys Val Thr His Ile Glu Ile Arg Asn Thr Arg
263          100          105          110
266 Asn Leu Thr Tyr Ile Asp Pro Asp Ala Leu Lys Glu Leu Pro Leu Leu
267          115          120          125
270 Lys Ser Leu Ala Phe Ser Asn Thr Gly Leu Lys Met Phe Pro Asp Leu

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274 Thr Lys Val Tyr Ser Thr Asp Ile Phe Phe Ile Leu Glu Ile Thr Asp
275 145      150      155      160
278 Asn Pro Tyr Met Thr Ser Ile Pro Val Asn Ala Phe Gln Gly Leu Cys
279      165      170      175
282 Asn Glu Thr Leu Thr Leu Lys Leu Tyr Asn Asn Gly Phe Thr Ser Val
283      180      185      190
286 Gln Gly Tyr Asp Phe Phe Gly Thr Lys Leu Asp Ala Val Tyr Leu Asn
287      195      200      205
290 Lys Asn Lys Tyr Leu Thr Val Ile Asp Lys Asp Ala Phe Gly Gly Val
291      210      215      220
294 Tyr Ser Gly Pro Ser Leu Asp Val Ser Gln Thr Ser Val Thr Ala
295 225      230      235      240
298 Leu Pro Ser Lys Gly Leu Glu His Leu Lys Glu Leu Ile Ala Arg Asn
299      245      250      255
302 Ser Trp Thr Leu Lys Lys Leu Ala Leu Ser Leu Ser Phe Leu His Leu
303      260      265      270
306 Thr Arg Ala Asp Leu Ser Tyr Pro Ser His Cys Cys Ala Phe Lys Asn
307      275      280      285
310 Gln Lys Lys Ile Arg Gly Ile Leu Glu Ser Leu Met Cys Asn Glu Ser
311      290      295      300
314 Ser Ile Glu Thr Leu Arg Gln Arg Lys Ser Val Asn Ala Leu Asn Ser
315 305      310      315      320
318 Pro Leu His Gln Glu Tyr Glu Glu Asn Leu Gly Asp Ser Ile Val Gly
319      325      330      335
322 Tyr Lys Glu Lys Ser Lys Phe Gln Asp Thr His Asn Asn Ala His Tyr
323      340      345      350
326 Tyr Val Phe Phe Glu Glu Gln Glu Asp Glu Ile Ile Gly Phe Gly Gln
327      355      360      365
330 Glu Leu Lys Asn Pro Gln Glu Thr Leu Gln Ala Phe Asp Ser His
331      370      375      380
334 Tyr Asp Tyr Thr Ile Cys Gly Asp Ser Glu Asp Met Val Cys Thr Pro
335 385      390      395      400
338 Lys Ser Asp Glu Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Lys Phe
339      405      410      415
342 Leu Arg Ile Val Val Trp Phe Val Ser Leu Leu Ala Leu Leu Gly Asn
343      420      425      430
346 Val Phe Val Leu Leu Ile Leu Leu Thr Ser His Tyr Lys Leu Asn Val
347      435      440      445
350 Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp Phe Cys Met Gly
351      450      455      460
354 Met Tyr Leu Leu Leu Ile Ala Ser Val Asp Leu Tyr Thr His Ser Glu
355 465      470      475      480
358 Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Pro Gly Cys Asn Thr
359      485      490      495
362 Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu
363      500      505      510
366 Thr Val Ile Thr Leu Glu Arg Trp Tyr Ala Ile Thr Phe Ala Met Ala
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